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In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 5, line 22, to page 6, line 3, and replace it with the following paragraph:

Fig. 2 shows the nucleotide sequence of cDNA (SEQ ID NO: 1) encoding MAH and its predicted amino acid sequence (SEQ ID NO: 2). In the amino acid sequence in Fig.2, the position of loop D is shown by the third underline (lowest underline), and in this loop, particularly 5 amino acids considered to exert a significant influence on binding to sugar chains are enclosed with a square. In the figure, I indicates an Xho I (ctcgag) restriction enzyme site, II indicates a Bgl II (agatct) restriction enzyme site, and III indicates an Spe I (actagt) restriction enzyme site.

Please delete the paragraph on page 6, lines 7-8, and replace it with the following paragraph:

Fig. 4 is an illustration of varieties of IgA1 sugar chain structures (SEQ ID NO: 34).

Please delete the paragraph on page 6, lines 9-10, and replace it with the following paragraph:

Fig. 5 shows the amino acid sequence of MAH loop C wherein the position of amino acid inserted by modification is indicated (SEQ ID NOS 35-37, respectively in order of appearance).

Please delete the paragraph on page 6, line 11, and replace it with the following paragraph:

Fig. 6 shows an outline of a phage display lectin library (SEQ ID NOS 38-39, respectively in order of appearance).

Please delete the paragraph on page 6, lines 20-23, and replace it with the following paragraph:

Fig. 9 shows amino acid sequences (SEQ ID NOS 38, and 22-31, respectively in order of appearance) of lectins contained in a lectin library used in discrimination of IgA different in sugar chain glycoform and in discrimination of cell subgroup derived from mesenchymal stem cells.

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Please delete the paragraph on page 7, lines 8-9, and replace it with the following paragraph:

Fig. 15 shows the amino acid sequence of MAII loop D, wherein the position of amino acid inserted by modification is indicated (SEQ ID NO: 40).

Please delete the paragraph on page 21, lines 11-22, and replace it with the following paragraph:

After it was confirmed that MAII lectin was expressed on phage to agglutinate erythrocyte, the sugar chain recognition site of loop C in MAH was modified randomly by AmpliTaq Gold DNA polymerase (manufactured by PE Biosystems) in a Perkin-Elmer 2400 thermal cycler. The primer and reverse primer used therein are shown in Table 1.

Table 1. Primers

Primer (containing an Eco RI site)

5' -

CCGGAATTCGACACTTACNNKNNKCATNNKNNKGATNNKNNKGACCCAAACTACAG
ACATATC-3' (SEQ ID NO: 32)

Reverse primer (containing a Bam HI site)

5'-CACAAACGAATGGGGATCCAC-3' (SEQ ID NO: 19)

Please delete the paragraph on page 23, lines 15-23, and replace it with the following paragraph:

Each modified MAH cDNA-pComb3 was subjected to PCR with a sense primer N-Flag-XhoI (5'- CCAGGTGAAACTGCTCGAGTCAGATG-3', SEQ ID NO: 20) and an antisense primer N-Flag-BglII (5'- TCCACCGCCAGATCTCTATGCAGTGTAACG-3', SEQ ID NO: 33). The resulting PCR product was recovered with a PCR Purification Kit (manufactured by QIAGEN) and treated with restriction enzymes Xho I And Bgl II. The product thus treated was ligated to XhoI/BglII-digested pFlag-ATS (manufactured by Sigma). Each plasmid thus obtained was incorporated into E. coli JM109.

Please delete the paragraph on page 35, lines 6-15, and replace it with the following paragraph:

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Table 5. Preparation of the vector

Composition of the PCR reaction solution (template (pFLAG-ATS), 1 μ l; primers (pFLAG-Spe I-sense 100 ng/ μ l and pFLAG-Spe I-anti 100 ng/ μ l), each 1.25 μ l; 10 x PCR buffer, 5 μ l; dNTP, 1 μ l; Milli Q, 40.5 μ l; and pfu turbo, 1 μ l)

PCR reaction conditions (95°C for 30 sec and 12 cycles [95°C for 30 sec, 55°C for 1 min and 68°C for 10 min])

Primer sequences

pFLAG-Spe I-sense: 5' - ccgggtaccctgcactagtagatagatgagctc (SEQ ID NO: 3)

FLAG-Spe I-anti: 5'-gagctcatctatctactagtcaggtaccctcg (SEQ ID NO: 4)

Please delete the paragraph on page 35, line 25, to page 36, line 11, and replace it with the following paragraph:

Table 6. Transformation with the vector

Composition of the PCR reaction solution (template 1.5 μ l; primers (N-Flag-XhoI, 100ng/ μ l and MAH-SpeI-anti, 100 ng/ μ l, each 0.5 μ l; dNTP, 4 μ l; 10 x PCR buffer, 5 μ l; Taq Gold, 1 μ l; and Milli Q 38.5 μ l)

The PCR reaction conditions were general (96°C for 5 min, 30 cycles [96°C for 1 min, 55°C for 1 min, 72°C for 2 min] and 72°C for 5 min)

Primer sequences

pFLAG-XhoI: 5'- ccagggtgaaactgctcgagtcagatg (SEQ ID NO: 5)

MAH-Spe I anti: 5'- tgggcaactagttgcagtgtaacgtgcg (SEQ ID NO: 6)

Primer sequences used in sequencing

N-26: 5'- catcataacggttcttgcaaatatc (SEQ ID NO: 7)

Loop D-Seq: 5'- gtaatatgcatctctagttaccc (SEQ ID NO: 8)

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Please delete the paragraph on page 36, line 21, to page 37, line 27, and replace it with the following paragraph:

A multicloning site Bgl II site could be converted into Spc I site. There was no mutation other than the target region. Theoretically predicted 120 modified MAHs could be isolated and identified.

Table 7. Primers used in random modification

N-Flag-XhoI: 5'- ccaggtgaaactgctcgagtcagatg (SEQ ID NO: 5)

LLD3: (SEQ ID NO: 9)

5'-ctacaagatctaaccatcgltgggtttcaactgcnnnlttaggagcacccgtggcagcaga

LLD4: (SEQ ID NO: 10)

5'- ctacaagatctaacatcgltgggtttcaactgctllmnnaggagcacccgtggcagcaga

LLD5: (SEQ ID NO: 11)

5'- ctacaagatctaaccatcgltgggtttcaactgctttaggmnnagcacccgtggcagcaga

LLD6: (SEQ ID NO: 12)

5'-ctacaagatctaaccatcggtgggtttcaactgctttaggagcmmnaccgtggcagcaga

Individually designed primers

MAH loop D-1Phe: (SEQ ID NO: 13)

5'-ctacaagatctaaccatcgltgggtttcaaaaactgctttaggagcacccgtggcagcaga

MAH loop D-2Asp: (SEQ ID NO: 14)

5'-ctacaagatctaaccatcgltgggtttcaacatcgtctttaggagcacccgtggcagcaga

MAH loop D-3Cys: (SEQ ID NO: 15)

5'- ctacaagatctaaccatcgltgggtttcaactgcacalltaggagcacccgtggcagcaga

MAH loop D-4Asp: (SEQ ID NO: 16)

5'- ctacaagatctaaccatcgltgggtttcaactgcttlatcaggagcacccgtggcagcaga

MAH loop D-6Phe: (SEQ ID NO: 17)

5'-ctacaagatctaaccatcgltgggtttcaactgctttaggagcaaaaccgtggcagcaga